

RAW SEQUENCE LISTING

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Application Serial Number: 10/590,953
Source: IFWP
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IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/590,953

DATE: 09/05/2006

TIME: 15:07:20

Input Set : E:\PC32090A_SEQUENCE LISTING.txt
 Output Set: N:\CRF4\09052006\J590953.raw

3 <110> APPLICANT: Pfizer Inc.; Pfizer Japan Inc.(for Japan)
 5 <120> TITLE OF INVENTION: GPR35
 7 <130> FILE REFERENCE: PC32099
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/590,953
 C--> 9 <141> CURRENT FILING DATE: 2006-08-28
 9 <160> NUMBER OF SEQ ID NOS: 23
 11 <170> SOFTWARE: PatentIn version 3.1
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 921
 15 <212> TYPE: DNA
 16 <213> ORGANISM: rat
 18 <400> SEQUENCE: 1
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 21 atctacttgg tcttgcgtct ggtgcgtggc ctgcgtctca atggcctggc actctggta 120
 23 ttctgcatac gcatgcacca gtggacggag acccgagtct atatgaccaa cctggctgtg 180
 25 gctgacgtct gcctgcgtctg ctccctgcca ttctgcgtgt actccctgaa atacagtact 240
 27 tcggacacac ccatactgcca gctctcacag ggcatctacc tggtaaacag gtacatgagc 300
 29 ataagcttgg tcaccggccat tgctgtggac cgctatgtgg cagtgcggca tccccctgcgt 360
 31 gcccgtgagc tgccgtcccc acggcaggct ggagcagtgt gtgtggccct ctgggtgata 420
 33 gtggtcacct ccctggtaact gcgctggcgc ctggggatac aggagggtgg cttctgcgtc 480
 35 agcagccaaa atcggtacaa cttcagcacc actgccttct cgctgctggg atttacactg 540
 37 ccgctggcca tagtggtctt ctgcgtttt caggttgtga ctgcgttggc ccgaaggcca 600
 39 gccactgacg tggagcaggt ggaggccact cagaaggcca cccgcattgtt ctggggccaac 660
 41 ttggccgtgt ttatcatctg ctccctgccc ctgcatttga tcctgacagt gcaggtctcc 720
 43 ctgaacctcc acacctgcgc tgcccgaac atcttcagcc gtgcctgac aatcacagcc 780
 45 aagctctcag acatcaactg ctgcctggat gccatctgtt actactacat ggccaaagag 840
 47 ttccaggatg cgtcctgctg ggccacagcc tctagcacac cccacaagag ccaagatact 900
 49 cagagcctga gcctcaccta g 921
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 53 <211> LENGTH: 306
 54 <212> TYPE: PRT
 55 <213> ORGANISM: rat
 57 <400> SEQUENCE: 2
 59 Met Asn Asn Thr Asn Cys Ser Ile Leu Pro Trp Pro Ala Ala Val Asn
 60 1 5 10 15
 63 His Ile Phe Thr Ile Tyr Leu Val Leu Leu Val Leu Gly Leu Leu
 64 20 25 30
 67 Leu Asn Gly Leu Ala Leu Trp Val Phe Cys Tyr Arg Met His Gln Trp
 68 35 40 45
 71 Thr Glu Thr Arg Val Tyr Met Thr Asn Leu Ala Val Ala Asp Val Cys
 72 50 55 60
 75 Leu Leu Cys Ser Leu Pro Phe Val Leu Tyr Ser Leu Lys Tyr Ser Thr
 76 65 70 75 80

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79 Ser Asp Thr Pro Ile Cys Gln Leu Ser Gln Gly Ile Tyr Leu Val Asn
80 85 90 95
83 Arg Tyr Met Ser Ile Ser Leu Val Thr Ala Ile Ala Val Asp Arg Tyr
84 100 105 110
87 Val Ala Val Arg His Pro Leu Arg Ala Arg Glu Leu Arg Ser Pro Arg
88 115 120 125
91 Gln Ala Gly Ala Val Cys Val Ala Leu Trp Val Ile Val Val Thr Ser
92 130 135 140
95 Leu Val Leu Arg Trp Arg Leu Gly Ile Gln Glu Gly Phe Cys Phe
96 145 150 155 160
99 Ser Ser Gln Asn Arg Tyr Asn Phe Ser Thr Thr Ala Phe Ser Leu Leu
100 165 170 175
103 Gly Phe Tyr Leu Pro Leu Ala Ile Val Val Phe Cys Ser Leu Gln Val
104 180 185 190
107 Val Thr Ala Leu Ala Arg Arg Pro Ala Thr Asp Val Glu Gln Val Glu
108 195 200 205
111 Ala Thr Gln Lys Ala Thr Arg Met Val Trp Ala Asn Leu Ala Val Phe
112 210 215 220
115 Ile Ile Cys Phe Leu Pro Leu His Leu Ile Leu Thr Val Gln Val Ser
116 225 230 235 240
119 Leu Asn Leu His Thr Cys Ala Ala Arg Asn Ile Phe Ser Arg Ala Leu
120 245 250 255
123 Thr Ile Thr Ala Lys Leu Ser Asp Ile Asn Cys Cys Leu Asp Ala Ile
124 260 265 270
127 Cys Tyr Tyr Tyr Met Ala Lys Glu Phe Gln Asp Ala Ser Leu Arg Ala
128 275 280 285
131 Thr Ala Ser Ser Thr Pro His Lys Ser Gln Asp Thr Gln Ser Leu Ser
132 290 295 300
135 Leu Thr
136 305
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140 <211> LENGTH: 930
141 <212> TYPE: DNA
142 <213> ORGANISM: human
144 <400> SEQUENCE: 3
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147 ctgggcttct acgcctactt gggcgtcctg ctggtgctag gcctgctgct caacagcctg 120
149 ggcctctggg tggctgtctg ccgcgtgcag cagtggacgg agaccgcatt ctacatgacc 180
151 aacctggcgg tggccgacct ctgcctgtctg tgccacccgt ccttcgtct gcactccctg 240
153 cgagacacct cagacacgccc gctgtgccag ctctccagg gcatctacct gaccaacagg 300
155 tacatgagca tcagccttgtt catggccatc ggcgtggacc gctatgtggc cgtgcggcac 360
157 cgcgtcggtt cccgcggct gcggtcccccc aggccaggctg cggccgtgtg cgcggctctc 420
159 tgggtgtctgg tcatcggtctc cctggtggtt cgtctggctcc tggggattca ggagggcggc 480
161 ttctgcttca ggagcaccccg gcacaatttc aactccatgg cgttcccgct gctggattc 540
163 tacctgcccc tggccgttgtt ggtcttctgc tccctgaagg tggtgactgc cctggccccag 600
165 aggccaccca cgcacgtggg gcaggcagag gccacccgca aggctgcccc catggctctgg 660
167 gccaacctcc tggtgttcgtt ggtctgtttc ctggccctgc acgtggggct gacagtgcgc 720
169 ctgcgactgg gctggAACGC ctgtggccctc ctggagacga tccgtcgcc cctgtacata 780
171 accagcaagc tctcagatgc caactgctgc ctggacgcca tctgctacta ctacatggcc 840

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179	<211>	LENGTH: 309																
180	<212>	TYPE: PRT																
181	<213>	ORGANISM: human																
183	<400>	SEQUENCE: 4																
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186	1																	900
																		930
187	5																	
188	10																	
189	15																	
190	20																	
191	25																	
192	30																	
193	Leu	Gly	Leu	Leu	Leu	Asn	Ser	Leu	Ala	Leu	Trp	Val	Phe	Cys	Cys	Arg		
194	35																	
195	40																	
196	45																	
197	Met	Gln	Gln	Trp	Thr	Glu	Thr	Arg	Ile	Tyr	Met	Thr	Asn	Leu	Ala	Val		
198	50																	
199	55																	
200	60																	
201	Ala	Asp	Leu	Cys	Leu	Leu	Cys	Thr	Leu	Pro	Phe	Val	Leu	His	Ser	Leu		
202	65																	
203	70																	
204	75																	
205	80																	
206	Arg	Asp	Thr	Ser	Asp	Thr	Pro	Leu	Cys	Gln	Leu	Ser	Gln	Gly	Ile	Tyr		
207	85																	
208	90																	
209	95																	
210	Leu	Thr	Asn	Arg	Tyr	Met	Ser	Ile	Ser	Leu	Val	Met	Ala	Ile	Ala	Val		
211	100																	
212	105																	
213	110																	
214	Asp	Arg	Tyr	Val	Ala	Val	Arg	His	Pro	Leu	Arg	Ala	Arg	Gly	Leu	Arg		
215	115																	
216	120																	
217	125																	
218	Ser	Pro	Arg	Gln	Ala	Ala	Ala	Val	Cys	Ala	Val	Leu	Trp	Val	Leu	Val		
219	130																	
220	135																	
221	140																	
222	Ile	Gly	Ser	Leu	Val	Ala	Arg	Trp	Leu	Leu	Gly	Ile	Gln	Glu	Gly	Gly		
223	145																	
224	150																	
225	155																	
226	160																	
227	Phe	Cys	Phe	Arg	Ser	Thr	Arg	His	Asn	Phe	Asn	Ser	Met	Ala	Phe	Pro		
228	165																	
229	170																	
230	Leu	Leu	Gly	Phe	Tyr	Leu	Pro	Leu	Ala	Val	Val	Val	Val	Phe	Cys	Ser	Leu	
231	180																	
232	185																	
233	190																	
234	Lys	Val	Val	Thr	Ala	Leu	Ala	Gln	Arg	Pro	Pro	Thr	Asp	Val	Gly	Gln		
235	195																	
236	200																	
237	205																	
238	Ala	Glu	Ala	Thr	Arg	Lys	Ala	Ala	Arg	Met	Val	Trp	Ala	Asn	Leu	Leu		
239	210																	
240	215																	
241	220																	
242	Val	Phe	Val	Val	Cys	Phe	Leu	Pro	Leu	His	Val	Gly	Leu	Thr	Val	Arg		
243	225																	
244	230																	
245	235																	
246	Leu	Ala	Val	Gly	Trp	Asn	Ala	Cys	Ala	Leu	Leu	Glu	Thr	Ile	Arg	Arg		
247	245																	
248	250																	
249	255																	
250	Ala	Leu	Tyr	Ile	Thr	Ser	Lys	Leu	Ser	Asp	Ala	Asn	Cys	Cys	Leu	Asp		
251	260																	
252	265																	
253	270																	
254	Ala	Ile	Cys	Tyr	Tyr	Tyr	Met	Ala	Lys	Glu	Phe	Gln	Glu	Ala	Ser	Ala		
255	275																	
256	280																	
257	285																	
258	Leu	Ala	Val	Ala	Pro	Ser	Ala	Lys	Ala	His	Lys	Ser	Gln	Asp	Ser	Leu		
259	290																	
260	295																	
261	300																	
262	Cys	Val	Thr	Leu	Ala													
263	305																	
264	265	<210>	SEQ ID NO: 5															
265	266	<211>	LENGTH: 924															

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267 <212> TYPE: DNA
 268 <213> ORGANISM: mouse
 270 <400> SEQUENCE: 5
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 275 gtattctgtc atcgcatgca ccagtggaca gagacccgca tctatatgac caacctggct 180
 277 .gtqqccggacc tctgcctgtc ctgctccttgc ccatttgtgc tgtactccct qaaatatagt 240
 279 tcttcagacat caccgtctg ccagctctca cagggcatct acctggccaa cagatacatg 300
 281 agcataagcc tggtaactgc cattgctgtg gaccgtatg tggcagtgcg gcatccccgt 360
 283 cgtgcgcgtg agctgcggc cccgagacag gctgcagcag tggcgtgtggc ccttgggtg 420
 285 atagtggtca cctccctgtt agtgcgttgg cgccctggga tgcaggaggg tggcttctgc 480
 287 ttcagcagcc aaacccggcg caatttcagc accactgcct tctcaactgtc gggattctac 540
 289 ctgccgcgtt ccategtgtt ttgcaggttag tgactgtgtc atcgagaagg 600
 291 ccagccgcgtt atgtggggca ggcagaggcc accaaaaagg ccacccacat ggtctggcc 660
 293 aacttggctg tgtttgtcat ctgcatttcctg cccttgcatttggccttgc cgtgcaggc 720
 295 tccctgaacc tcaatacctt tgctgtccca gacacccat tgcgtgccttgc gtcacatcaca 780
 297 ggtaaaactct cagacaccaa ctgcgtgccttgc gatccatct ttactacta catggccaga 840
 299 gagttccagg aagcgtccaa gccagccacg tcttccaaca caccccacaa gagccaagat 900
 301 tcccaagatccc tgagcctcac ctag 924
 304 <210> SEQ ID NO: 6
 305 <211> LENGTH: 307
 306 <212> TYPE: PRT
 307 <213> ORGANISM: mouse
 309 <400> SEQUENCE: 6
 311 Met Asn Ser Thr Thr Cys Asn Ser Thr Leu Thr Trp Pro Ala Ser Val
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 315 Asn Asn Phe Phe Ile Ile Tyr Ser Ala Leu Leu Leu Val Leu Gly Leu
 316 20 25 30
 319 Leu Leu Asn Ser Val Ala Leu Trp Val Phe Cys Tyr Arg Met His Gln
 320 35 40 45
 323 Trp Thr Glu Thr Arg Ile Tyr Met Thr Asn Leu Ala Val Ala Asp Leu
 324 50 55 60
 327 Cys Leu Leu Cys Ser Leu Pro Phe Val Leu Tyr Ser Leu Lys Tyr Ser
 328 65 70 75 80
 331 Ser Ser Asp Thr Pro Val Cys Gln Leu Ser Gln Gly Ile Tyr Leu Ala
 332 85 90 95
 335 Asn Arg Tyr Met Ser Ile Ser Leu Val Thr Ala Ile Ala Val Asp Arg
 336 100 105 110
 339 Tyr Val Ala Val Arg His Pro Leu Arg Ala Arg Glu Leu Arg Ser Pro
 340 115 120 125
 343 Arg Gln Ala Ala Ala Val Cys Val Ala Leu Trp Val Ile Val Val Thr
 344 130 135 140
 347 Ser Leu Val Val Arg Trp Arg Leu Gly Met Gln Glu Gly Gly Phe Cys
 348 145 150 155 160
 351 Phe Ser Ser Gln Thr Arg Arg Asn Phe Ser Thr Thr Ala Phe Ser Leu
 352 165 170 175
 355 Leu Gly Phe Tyr Leu Pro Leu Ala Ile Val Val Phe Cys Ser Leu Gln
 356 180 185 190
 359 Val Val Thr Val Leu Ser Arg Arg Pro Ala Ala Asp Val Gly Gln Ala

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360	195	200	205	
363	Glu Ala Thr Gln Lys Ala Thr His Met Val Trp Ala Asn Leu Ala Val			
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367	Phe Val Ile Cys Phe Leu Pro Leu His Val Val Leu Thr Val Gln Val			
368	225	230	235	240
371	Ser Leu Asn Leu Asn Thr Cys Ala Ala Arg Asp Thr Phe Ser Arg Ala			
372	245	250	255	
375	Leu Ser Ile Thr Gly Lys Leu Ser Asp Thr Asn Cys Cys Leu Asp Ala			
376	260	265	270	
379	Ile Cys Tyr Tyr Tyr Met Ala Arg Glu Phe Gln Glu Ala Ser Lys Pro			
380	275	280	285	
383	Ala Thr Ser Ser Asn Thr Pro His Lys Ser Gln Asp Ser Gln Ile Leu			
384	290	295	300	
387	Ser Leu Thr			
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392	<211> LENGTH: 61			
393	<212> TYPE: DNA			
394	<213> ORGANISM: Artificial Sequence			
396	<220> FEATURE:			
397	<223> OTHER INFORMATION: primer			
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406	<211> LENGTH: 30			
407	<212> TYPE: DNA			
408	<213> ORGANISM: Artificial Sequence			
410	<220> FEATURE:			
411	<223> OTHER INFORMATION: primer			
413	<400> SEQUENCE: 8			
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418	<211> LENGTH: 36			
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422	<220> FEATURE:			
423	<223> OTHER INFORMATION: primer			
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430	<211> LENGTH: 40			
431	<212> TYPE: DNA			
432	<213> ORGANISM: Artificial Sequence			
434	<220> FEATURE:			
435	<223> OTHER INFORMATION: primer			
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VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date